Detection of novel antimicrobial resistance genes in oil contaminated soils by metagenomic functional analysis

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Our ability to cure infections that were once considered benign or of low risk is at stake due to the development and spread of antimicrobial resistance mechanisms (AMR). One of the measures proposed to fight this problem is the research aimed at detection and molecular characterisation of the AMR to design strategies to combat them. In this regard, metagenomic functional analyses are powerful tools to detect new AMR genes in different environments.

In this work, we have searched for genes that confer resistance to different antibiotics used in hospitals by following a metagenomics approach. We have screened two metagenomic libraries, previously constructed in our laboratory, from two different locations. In order to overcome the inherent limitation of expressing heterologous genes from long DNA fragments in *E. coli*, we have used a fosmid vector that allows processive transcription of long stretches of environmental DNA by using two viral transcriptional machineries. One is based on the phage T7 RNA-polymerase, which are insensitive to many of the bacterial transcription terminators. The second system involves the use of the lambda N-anti-termination protein coupled to a salicylate inducible promoter. We have searched for fosmids from both libraries that are resistant to different groups of antibiotics used in hospitals. Although we could not find any fosmid conferring resistance to polimixins or fluoroquinolons, we have detected clones resistant to cephalosporins (ceftriaxone and cefixime) and carbapenems (meropenem and imipenem) bearing fosmids that code for extended spectrum b-lactamases, metallo-b-lactamases and/or efflux pumps.

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